

SEQUENCE LISTING

<110> BAYER AG

<120> Use of VLCFAE for identifying herbicidally active compounds

<130> Le A 34 730

<140>

<141>

<160> 2

<170> PatentIn Ver. 2.1

<210> 1

<211> 2782

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (176) .. (583)

$\langle 220 \rangle$

<221> CDS

<222> (1119) .. (1745)

 $\langle 220 \rangle$

<221> CDS

<222> (1821) .. (2438)

<400> 1

acattaacta cctctcacca accaccaaac ccaatcccca caatattacc attactctca 60

tataactaca catattcata tttacatttt ttgccaacac aactccttat aagatatata
120

cttcatcaac ctatagatct cactcacata atcaacctac aaaacaaaaa caaga atg
178

Met
1

ggt aga tcc aac gag caa gat ctg ctc tct acc gag atc gtt aat cgt
226

Gly Arg Ser Asn Glu Gln Asp Leu Leu Ser Thr Glu Ile Val Asn Arg
5 10 15

ggg atc gaa cca tcc ggt cct aac gcc ggc tca cca acg ttc tcg gtt
274

Gly Ile Glu Pro Ser Gly Pro Asn Ala Gly Ser Pro Thr Phe Ser Val
20 25 30

agg gtc agg aga cgt ttg cct gat ttt ctt cag tcg gtg aac ttg aag
322

Arg Val Arg Arg Arg Leu Pro Asp Phe Leu Gln Ser Val Asn Leu Lys
35 40 45

tac gtg aaa ctt ggt tac cac tac ctc ata aac cat gcg gtt tat ttg
370

Tyr Val Lys Leu Gly Tyr His Tyr Leu Ile Asn His Ala Val Tyr Leu
50 55 60 65

gcg acc ata ccg gtt ctt gtg ctg gtt ttt agt gct gag gtt ggg agt
418
Ala Thr Ile Pro Val Leu Val Leu Val Phe Ser Ala Glu Val Gly Ser
70 75 80

tta agc aga gaa gag att tgg aag aag ctt tgg gac tat gat ctt gca
466
Leu Ser Arg Glu Glu Ile Trp Lys Lys Leu Trp Asp Tyr Asp Leu Ala
85 90 95

act gtt atc gga ttc ttc ggt gtc ttt gtt tta acc gct tgt gtc tac
514
Thr Val Ile Gly Phe Phe Gly Val Phe Val Leu Thr Ala Cys Val Tyr
100 105 110

ttc atg tct cgt cct cgc tct gtt tat ctt att gat ttc gct tgt tac
562
Phe Met Ser Arg Pro Arg Ser Val Tyr Leu Ile Asp Phe Ala Cys Tyr
115 120 125

aag ccc tcc gat gaa cac aag gtacgtccca actttttccat agaggaaata
613
Lys Pro Ser Asp Glu His Lys
130 135

gtctaaatta cttttaccca aaaaaaaaaa aaaaaaaaaa atctaaatta agtataactta
673

agaaattata attagatttg tcaaaaaata ataattataa ttagatggat tagttgttta
733

tagggctgcc taaataaaat aaaattttgc ctttgcattg gttacgttag taattatttt
793

tcaggtatat ataaaaagta attattttgc aaaaccttta gatattgggtt acgtttgatt
853

taaaaccgaa tggtttcgta gaaatttgag aaagtagata acctaaaaac tccgattaaa
913

gaaaccgggtt tgacttatat aatttttaact ggtttctggtt ttcatttttat tttataaaaa
973

aaacaatcca aattttacgac ctataatcaa aggagattga taggaaccgg actgataatt
1033

aatgaagct gaatcaaacc aaacaaaagt tcattttaatt ccggttctct cgggtttaatt
1093

ctcttttttg attggattgg tttag gtg aca aaa gaa gag ttc ata gaa cta
1145
Val Thr Lys Glu Glu Phe Ile Glu Leu
140 145

gcg aga aaa tca ggg aag ttc gac gaa gag aca ctc ggt ttc aag aag
1193
Ala Arg Lys Ser Gly Lys Phe Asp Glu Glu Thr Leu Gly Phe Lys Lys
150 155 160

agg atc tta caa gcc tca ggc ata ggc gac gag aca tac gtc cca aga
1241
Arg Ile Leu Gln Ala Ser Gly Ile Gly Asp Glu Thr Tyr Val Pro Arg

165	170	175
tcc atc tct tca tca gaa aac ata aca acg atg aaa gaa ggt cgt gaa 1289		
Ser Ile Ser Ser Ser Glu Asn Ile Thr Thr Met Lys Glu Gly Arg Glu 180 185 190		
gaa gcc tct aca gtg atc ttt gga gca cta gac gaa ctc ttc gag aag 1337		
Glu Ala Ser Thr Val Ile Phe Gly Ala Leu Asp Glu Leu Phe Glu Lys 195 200 205		
aca cgt gta aaa cct aaa gac gtt ggt gtc ctt gtg gtt aac tgt agc 1385		
Thr Arg Val Lys Pro Lys Asp Val Gly Val Leu Val Val Asn Cys Ser 210 215 220 225		
att ttc aac ccg aca ccg tcg ttg tcc gca atg gtg ata aac cat tac 1433		
Ile Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Ile Asn His Tyr 230 235 240		
aag atg aga ggg aac ata ctt agt tac aac ctt gga ggg atg gga tgt 1481		
Lys Met Arg Gly Asn Ile Leu Ser Tyr Asn Leu Gly Gly Met Gly Cys 245 250 255		
tcg gct gga atc ata gct att gat ctt gct cgt gac atg ctt cag tct 1529		
Ser Ala Gly Ile Ile Ala Ile Asp Leu Ala Arg Asp Met Leu Gln Ser 260 265 270		
aac cct aat agt tat gct gtt gtt gtg agt act gag atg gtt ggg tat 1577		
Asn Pro Asn Ser Tyr Ala Val Val Val Ser Thr Glu Met Val Gly Tyr 275 280 285		
aat tgg tac gtg gga agt gac aag tca atg gtt ata cct aat tgt ttc 1625		
Asn Trp Tyr Val Gly Ser Asp Lys Ser Met Val Ile Pro Asn Cys Phe 290 295 300 305		
ttt agg atg ggt tgt tct gcc gtt atg ctc tct aac cgt cgt cgt gac 1673		
Phe Arg Met Gly Cys Ser Ala Val Met Leu Ser Asn Arg Arg Arg Asp 310 315 320		
ttt cgc cat gct aag tac cgt ctc gag cac att gtc cga act cat aag 1721		
Phe Arg His Ala Lys Tyr Arg Leu Glu His Ile Val Arg Thr His Lys 325 330 335		
gct gct gac gac cgt agc ttc agg tttcattcat tttggtatta attcgtttta 1775		
Ala Ala Asp Asp Arg Ser Phe Arg 340 345		
caatctcttg accgacctag taactaattt tgtgtggttt ttagg agt gtg tac cag 1832		
		Ser Val Tyr Gln
gaa gaa gat gaa caa gga ttc aag ggg ttg aag ata agt aga gac tta 1880		

Glu Glu Asp Glu Gln Gly Phe Lys Gly Leu Lys Ile Ser Arg Asp Leu
 350 355 360 365
 atg gaa gtt gga ggt gaa gct ctc aag aca aac atc act acc tta ggt
 1928
 Met Glu Val Gly Gly Glu Ala Leu Lys Thr Asn Ile Thr Thr Leu Gly
 370 375 380
 cct ctt gtc cta cct ttc tcc gag cag ctt ctc ttc ttt gct gct ttg
 1976
 Pro Leu Val Leu Pro Phe Ser Glu Gln Leu Leu Phe Phe Ala Ala Leu
 385 390 395
 ctc cgc cga aca ttc tca cct gct gcc aaa acg tcc aca acc act tcc
 2024
 Leu Arg Arg Thr Phe Ser Pro Ala Ala Lys Thr Ser Thr Thr Thr Ser
 400 405 410
 ttc tct act tcc gcc acc gca aaa acc aat gga atc aag tct tcc tct
 2072
 Phe Ser Thr Ser Ala Thr Ala Lys Thr Asn Gly Ile Lys Ser Ser Ser
 415 420 425
 tcc gat ctg tcc aag cca tac atc ccg gac tac aag ctc gcc ttc gag
 2120
 Ser Asp Leu Ser Lys Pro Tyr Ile Pro Asp Tyr Lys Leu Ala Phe Glu
 430 435 440 445
 cat ttt tgc ttc cac gcg gca agc aaa gta gtg ctt gaa gag ctt caa
 2168
 His Phe Cys Phe His Ala Ala Ser Lys Val Val Leu Glu Glu Leu Gln
 450 455 460
 aag aat cta ggc ttg agt gaa gag aat atg gag gct tct agg atg aca
 2216
 Lys Asn Leu Gly Leu Ser Glu Glu Asn Met Glu Ala Ser Arg Met Thr
 465 470 475
 ctt cac agg ttt gga aac act tct agc agt gga atc tgg tat gag ttg
 2264
 Leu His Arg Phe Gly Asn Thr Ser Ser Ser Gly Ile Trp Tyr Glu Leu
 480 485 490
 gct tac atg gag gcc aag gaa agt gtt cgt aga ggc gat agg gtt tgg
 2312
 Ala Tyr Met Glu Ala Lys Glu Ser Val Arg Arg Gly Asp Arg Val Trp
 495 500 505
 cag atc gct ttc ggt tct ggt ttt aag tgt aac agt gtg gtg tgg aag
 2360
 Gln Ile Ala Phe Gly Ser Gly Phe Lys Cys Asn Ser Val Val Trp Lys
 510 515 520 525
 gca atg agg aag gtg aag aag cca acc agg aac aat cct tgg gtg gat
 2408
 Ala Met Arg Lys Val Lys Lys Pro Thr Arg Asn Asn Pro Trp Val Asp
 530 535 540
 tgc atc aac cgt tac cct gtg cct ctc taa attatcattc ttctaaatta
 2458
 Cys Ile Asn Arg Tyr Pro Val Pro Leu
 545 550

<400>	2															
Met	Gly	Arg	Ser	Asn	Glu	Gln	Asp	Leu	Leu	Ser	Thr	Glu	Ile	Val	Asn	
1				5					10					15		
Arg	Gly	Ile	Glu	Pro	Ser	Gly	Pro	Asn	Ala	Gly	Ser	Pro	Thr	Phe	Ser	
			20					25					30			
Val	Arg	Val	Arg	Arg	Arg	Leu	Pro	Asp	Phe	Leu	Gln	Ser	Val	Asn	Leu	
		35					40					45				
Lys	Tyr	Val	Lys	Leu	Gly	Tyr	His	Tyr	Leu	Ile	Asn	His	Ala	Val	Tyr	
	50					55					60					
Leu	Ala	Thr	Ile	Pro	Val	Leu	Val	Leu	Val	Phe	Ser	Ala	Glu	Val	Gly	
65					70					75					80	
Ser	Leu	Ser	Arg	Glu	Glu	Ile	Trp	Lys	Lys	Leu	Trp	Asp	Tyr	Asp	Leu	
				85					90					95	-	
Ala	Thr	Val	Ile	Gly	Phe	Phe	Gly	Val	Phe	Val	Leu	Thr	Ala	Cys	Val	
			100					105					110			
Tyr	Phe	Met	Ser	Arg	Pro	Arg	Ser	Val	Tyr	Leu	Ile	Asp	Phe	Ala	Cys	
		115					120					125				
Tyr	Lys	Pro	Ser	Asp	Glu	His	Lys	Val	Thr	Lys	Glu	Glu	Phe	Ile	Glu	
	130					135					140					
Leu	Ala	Arg	Lys	Ser	Gly	Lys	Phe	Asp	Glu	Glu	Thr	Leu	Gly	Phe	Lys	
145					150					155					160	
Lys	Arg	Ile	Leu	Gln	Ala	Ser	Gly	Ile	Gly	Asp	Glu	Thr	Tyr	Val	Pro	
				165					170					175		
Arg	Ser	Ile	Ser	Ser	Ser	Glu	Asn	Ile	Thr	Thr	Met	Lys	Glu	Gly	Arg	
			180					185					190			
Glu	Glu	Ala	Ser	Thr	Val	Ile	Phe	Gly	Ala	Leu	Asp	Glu	Leu	Phe	Glu	
		195					200					205				

Lys	Thr	Arg	Val	Lys	Pro	Lys	Asp	Val	Gly	Val	Leu	Val	Val	Asn	Cys
210						215					220				
Ser	Ile	Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Ile	Asn	His
225					230					235					240
Tyr	Lys	Met	Arg	Gly	Asn	Ile	Leu	Ser	Tyr	Asn	Leu	Gly	Gly	Met	Gly
				245					250					255	
Cys	Ser	Ala	Gly	Ile	Ile	Ala	Ile	Asp	Leu	Ala	Arg	Asp	Met	Leu	Gln
			260					265					270		
Ser	Asn	Pro	Asn	Ser	Tyr	Ala	Val	Val	Val	Ser	Thr	Glu	Met	Val	Gly
		275					280					285			
Tyr	Asn	Trp	Tyr	Val	Gly	Ser	Asp	Lys	Ser	Met	Val	Ile	Pro	Asn	Cys
	290					295					300				
Phe	Phe	Arg	Met	Gly	Cys	Ser	Ala	Val	Met	Leu	Ser	Asn	Arg	Arg	Arg
305					310					315					320
Asp	Phe	Arg	His	Ala	Lys	Tyr	Arg	Leu	Glu	His	Ile	Val	Arg	Thr	His
				325					330					335	
Lys	Ala	Ala	Asp	Asp	Arg	Ser	Phe	Arg	Ser	Val	Tyr	Gln	Glu	Glu	Asp
			340					345					350		
Glu	Gln	Gly	Phe	Lys	Gly	Leu	Lys	Ile	Ser	Arg	Asp	Leu	Met	Glu	Val
		355					360					365			
Gly	Gly	Glu	Ala	Leu	Lys	Thr	Asn	Ile	Thr	Thr	Leu	Gly	Pro	Leu	Val
	370					375					380				
Leu	Pro	Phe	Ser	Glu	Gln	Leu	Leu	Phe	Phe	Ala	Ala	Leu	Leu	Arg	Arg
385					390					395					400
Thr	Phe	Ser	Pro	Ala	Ala	Lys	Thr	Ser	Thr	Thr	Thr	Ser	Phe	Ser	Thr
				405					410					415	
Ser	Ala	Thr	Ala	Lys	Thr	Asn	Gly	Ile	Lys	Ser	Ser	Ser	Ser	Asp	Leu
			420					425						430	
Ser	Lys	Pro	Tyr	Ile	Pro	Asp	Tyr	Lys	Leu	Ala	Phe	Glu	His	Phe	Cys
		435					440					445			
Phe	His	Ala	Ala	Ser	Lys	Val	Val	Leu	Glu	Glu	Leu	Gln	Lys	Asn	Leu
	450					455					460				
Gly	Leu	Ser	Glu	Glu	Asn	Met	Glu	Ala	Ser	Arg	Met	Thr	Leu	His	Arg
465					470					475					480
Phe	Gly	Asn	Thr	Ser	Ser	Ser	Gly	Ile	Trp	Tyr	Glu	Leu	Ala	Tyr	Met
				485					490					495	
Glu	Ala	Lys	Glu	Ser	Val	Arg	Arg	Gly	Asp	Arg	Val	Trp	Gln	Ile	Ala
			500					505					510		
Phe	Gly	Ser	Gly	Phe	Lys	Cys	Asn	Ser	Val	Val	Trp	Lys	Ala	Met	Arg
		515					520					525			
Lys	Val	Lys	Lys	Pro	Thr	Arg	Asn	Asn	Pro	Trp	Val	Asp	Cys	Ile	Asn
	530					535					540				

Arg Tyr Pro Val Pro Leu
545 550

FOUO 4595060